

1 AGATGAGTGT GGGGGTGA AGAGTCAAGT TCGGGGCT  
 METSerVal GlyArgArg ArgValLysLeu LeuGlyIle  
 41 CCGATGATG GCAAAGTCT TCATTATTT GATGIGGAA  
 eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu  
 81 GTCTCCAAA ACAGTAGCA AGACAAAAT CGAAGGGAG  
 ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG  
 121 GGTATATAT CCGAAGAG AGGTCTGCA AGCCACCCAG  
 lyValIleIle ProLysGlu LysPheTrpLys ProProSe  
 161 CAGTCCCGG GGTACTGCA ACAGGGACA GGAAGCTG  
 rThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu  
 201 AACAGTGGT ACAATCCCT CTGACAGG GTGGCCATC  
 AsnArgTrpTyr AsnProIle LeuAsnArg ValAlaAsnG  
 241 AGACAGGGA GGTAGGACA TCTCCAAACA CAGTCACT  
 lThrGlyGlu LeuAlaThr SerProAsnThr SerHisLe  
 281 GGCATTTGT GAAACAGCT CGAGGTGAT GACAGCTG  
 uSerTyrCys GluProAspSer ThrValMET ThrAlaVal  
 321 ACAGATTTA ATATCTGCC GGCAGATTT AAAGACTTC  
 ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPheL  
 361 TCTGTATTT GAGTGGCGG AATTACTGCC TCGTATAGA  
 euLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs  
 401 TCAACCGAG AAATGTCAA AGAGCCCTT CTACTATTG  
 pGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu  
 441 CGATAAAGT CCGTATTCC ACATTTGCC AGAAGGCCAG  
 AlaIleLysSer LeuIlePro HisPheAla ArgArgGlnA  
 481 CAATCCGGA GTCTGGGGC CGGAAACA ACCTAGGGA  
 laIleArgGlu SerTrpGly ArgGluThrAsn ValGlyAs  
 521 CCGACAGTA GTGAGGGCT TCGGTGCGG CAGACACC  
 nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro  
 561 CCGAGGACA ACCACCTCA CTTTGGGAC ATGCTAAGT  
 ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP  
 601 TTGAGGTGA CAGCACCCG GACATCTCA TGTGGACTA  
 heGluSerAsp LysHisGln AspIleLeuMET TrpAsnTy  
 641 TAGAGACACA TCTTCAACC TGCCCTGAA GGAGTCTG  
 rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu

FIG. 1 (sheet 1 of 2)

641 TTTCCTAGGT GGGTGGGAC TTCTGTCCA GAGCGAGT  
 PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP  
 721 TTGTCTTCAA GGGCATGAT GAGGTTTTC TGAACACCA  
 heValPheLys GlyAspAsp AspValPheVal AsnThrHi  
 761 TCACATCCTT AATTACTTCA ATAGCTTATC CAAGAGCAAA  
 sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys  
 801 GCGAAGACT TGTTCATAGG TGGGTGATC CACAATGCTG  
 AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG  
 841 GGGCTCAGG GGTATAGAA CTCAGTACT ACATCCGAGA  
 LyProHisArg AspLysLys LeuLysTyrTyr IleProGl  
 881 AGTCTCTTAC ACCGGGCTT ACCACGCTA TCGGGGGCT  
 uValPheTyr ThrGlyValTyr ProProTyr AlaGlyGly  
 921 GGTGGTTCC TGTACCCCG GGGGTTCC TTGAGGCTT  
 GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT  
 961 ACAGTCCGAC TGGGGGGTC CTCCTCTCC CTATTGATCA  
 yrSerAlaThr SerArgVal HisLeuTyrPro IleAspAs  
 1001 TGTCTATAG CCAATGTGCC TTGAGAACT GGGCTTGT  
 pValTyrThr GlyMetCysLeu GlnLysLeu GlyLeuVal  
 1041 CCGAGAGGC ACAAGGCTT CAGACATTT GATATTGAG  
 ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG  
 1081 AGAAAAATAA GAAAAATATT TGTCTCTATA TAGCCTAAT  
 LuLysAsnLys LysAsnIle CysSerTyrIle AspLeuME  
 1121 GTTAGTACAT AGCAGAAAC CTCAGAGAT GATTGATATC  
 TLeuValHis SerArgLysPro GlnGluMET IleAspIle  
 1161 TGTCTCTAGT TCGAAGTCC TAATTAAAA TGTCTA  
 TrpSerGlnLeu GlnSerPro AsnLeuLys Cys

FIG. 1 (sheet 2 of 2)

```

MAX--PQKV-----L-LR-LL--V
      10              20              30
MSVGP-RRV-----K-L
MA--S-SC-----Y-
MAP-----AVLTALPNRMSLPS-KWSL
MQSKHRL-----LFCIL--V
MLQWPRRHCCFAKMTWNAKRSIFPTHITIGV

LSLVKLLXXXFXFLKH--W-----
      40              50              60
LGILMMANV-IV-IVEVSKNSSQDKNGKGG
LSVVC-----ASA-----
L-----LSLLSLV-----
LPLILLVVGYCGLITHLH-----
LSIVFFIFAMELEFN-HD-LPGRAGFKENPV

--F--F--D-----TWY
      70              80              90
VIIPKEK-EWK-PSTPRAYWNREQEKLNRWY
-----LWY
ELNFERH-HY-
TYTERG-ERSTKSETNHSSLR-----NKK
LSIP--LRPQTGSXSXSXXLSHL-Y-----N
      100             110             120
NPILNRVANGT-ELATSPNTSHLSMCEPDS
LSIT--P-TS-YTG-KPFSHI-----
LSLPHY-----
-----ENDDTGGGA-SGLDKFAV-----
ETVPOQLPPOTATNENNTDLSPOQGVGTLES
TVXRYNXXFXNNXXTP-----PINSXXFEF
      130             140             150
TVMTAVTDFFNNLPDFFKDFLLYLRCRNYSL
TVARKNFTFGNIRTS-----PHSPEE
VIEPVNWMYF-IEYE-----LYRQDFRF
-----LRVPEFTAHV
TLSANGSIY-EKGIG-----HPNHYH-KY
LIDEPYKCKKK-PFLVLLIKSXPGXFXARQ
      160             170             180
LIPQFKKCAK-PFEL-AIP-LIPHARRC
LINEFNCEFNIPFLI-ISTTHKE-DARC
TLRFHSN-SHQNEFLIVT-RHSDVKARC
PVGQEAR-----TMEI-AVGNRRPE
LINEFEKQEQE-SPEEI-IAAEEQIEER
AIRETWGXEXNFXGIXVXRVELLGKXA-EX
      190             200             210
AIRE-SWGRETNVGNOTVVEVFLLGFTTPED
AIRETWGDFNNHKGK-KIATLFLLGNN-
AIPVTWGEKKSWWGYEMLTFELLCQQA-FR
AIFRTWGYEGRESDVHLRVELLGTAEDESE
SIFQTWGNFSLAPG-QIT-IFELLSI--K
XDPXLXXMVEXESRXHGDIIQQDFLDITYFN
      220             230             240
NHEDLSDMLKFEEDKQDILMWNRYR-FFR
-LFVLNQMVQESQIFHDIIVED-IDSYHN
E-KTIALSLFDEHVLVJDI-RDDFISTYNN
KQ-----AWESH-EHCDILCADSTCAYEN
LNGYIQRAILEESRQYHDTIOGEYIDTYVY
LTLKTLMGMRWVATFCPXA EYVMKTDSDVF
      250             260             270
SLKEVLFLLRWASISCHDAF-FVFGLDOMF
LTKTTEGMRWVATFCISKAKYVWVAD-EIF
LTKTIFAFRWMEFCNAKVIMKTTTDMF
NTLKTMLGHPWASEQFNRSFYLFLVLD EYY
LTKTLMGMNWVATYCHHIPVWVWVDSHMF
VNTXNLLNKLKPSLSHRXXLFTGY-VIXG
      280             290             300
VNTHHIINHYLNSLCKKAKKD-FIG-DVIHN
VNMONLIYHLL-ESTKP-RRYFTGY-VIN-
IN-GNIVKYL--N-NHSEKFFFTVPLTDN
VSAKNVIKFLGRGROFQOPELFAGHAFQT
VNT EYHINERHID-PP-HNY-ETN-LMR-

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FIG. 2 (sheet 1 of 2)

YGPYRDKFSKWTXKDLYPFVYPPYCSGG  
 310 320 330  
 AGFHRDRLKLYYFVFLT-GYPPVAGG  
 -GIRIVRRSKWYMERIY:DSNVPPFUSST  
 S-YPGFHHKNNHISYQEVPIKWFPPVCCCL  
 -SILFHKFSKWTVSLEEVPPDRWPPVTA  
 VAFNENFDSKWTMIFPLVFSERVEVF  
 T  
 GYIFSGDLAERLYKASLHVRLHLEDVYVG  
 340 350 360  
 FLYCPIALHISSTSRHLYPID  
 VIVSALVALLIYT  
 HCGDVPVYEMMSKPIKF  
 AFGLSOKALROAVLPPFRFD  
 VVGNNAKIFVGI  
 ICLXKLGIDPXXPXG--FNHW-KXXKSXC  
 370 380 390  
 MCLQKLGVLVEKHKCFRTSDISEKKNKNIC  
 LCLRLGLHGFQNSQ--FNHW-FMAYLC  
 -YNLHKVTHICEDTNLFFLY-RIHLDV  
 VALHAGISLOHCDD--RFHRPAYGPD  
 IANRITDVPFPNEFV--RVSYST  
 SYSRVIAV4OF-SPEEMIRIWNXL-Q-KNL  
 400 410 420  
 YIDLMLVSR-KQENDDISQI-SP  
 RYRRVITVHAI-UPHEHPIHDMSSKH  
 OLRPVIAHGF-SKEITTFQVML--RT  
 YSSVITASHFGDPEETVWE--  
 KYCHLITSHGF-QISELTKYHMHQNH  
 XC-----Y-----  
 430  
 KCC  
 RCC  
 TCC-----H  
 -CC-----RSANY-----A  
 ACANAAKEXAGRVRHRKLH

FIG. 2 (sheet 2 of 2)

FIG. 3

ATGATTTCGC CTCACGCTTT ACTGGTATT TTAGAAATT  
 METIleOysPro SerAlaLeu LeuValIle LeuArgAsnL  
 41 TATACGGGA AGAAAAATC ATTTCACAG AGATCCTCA  
 eIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs  
 81 TTGATTGAA TTAGGATGA AAAAGGGAA TATTCAGTTC  
 nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu  
 121 ACAACTCTG CAATCAGTGA TGCATTAAA GAAATCGATA  
 ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS  
 161 GTAGTGTGCT CAATGTGCT GTACAGGGG AGAGGGGATC  
 erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe  
 201 AGGGAGTCC AGCTTCATCA ATACCTGAG AGGCATTGGG  
 rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly  
 241 AATGAGAAG AGGTGCTCC TAAACTGGG GTGGTGGAGG  
 AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV  
 281 TACCATCGA AGACATCCA TACAACACC CCAATATACC  
 alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr  
 321 CAATGGGTT TTTCGGGAC TGGCTGGAT TGGAGGACA  
 cAsnValVal PheTyrAspLeu ProGlyIle GlySerThr  
 361 AATTTCGAC CAAACACTA CCGGAGAAA ATGAAGTCT  
 AsnPheProPro AsnThrTyr LeuGluLys METLysPheT  
 401 ATGAGTAGA TTCTTCATT ATTATTTCG CACAGGCTT  
 yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh  
 441 CAGAAAAAT GATATAGCA TTGCCAAGC AATCAGCATG  
 eLysLysAsn AspIleAspIle AlaLysAla IleSerMET  
 481 ATGAGAAGG AATCTACTT CCGCAGAAC AGGTGGACT  
 METLysLysGlu PheTyrPhe ValArgThr LysValAspS  
 521 CTGACATAAC AATGAGCA GATGGCAAC CTCAAACCTT  
 erAspIleThr AsnGluAla AspGlyLysPro GlnThrPh  
 561 TGCAGAGAA AGGTCTCC AGGACATCC CCTTAAGTCT  
 eAspLysGlu LysValLeuGln AspIleArg LeuAsnOys  
 601 CTGACACCTT TTAGGGGAA TGGCATTCCT GAGCCACAA  
 ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI  
 641 TCTTCTGCT CTCTACAAA AATGTTTGT ACTATGACTT  
 lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh

FIG. 4 (sheet 1 of 2)

581 CCCCCCTCCG ATGGACAAGC TCATAAGTGA CCCCCCTATC  
 eProValLeu METAspLysLeu IleSerAsp LeuProIle  
 721 TCCAGGAGAC ACAATTTTAT GCCTCCCTTA CCCAATATCA  
 TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT  
 761 CAGATTCAGT CATGAAAAG AAGGCGCAAT TTCGCAAGCA  
 hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGI  
 801 RAGGATTTCG CTGGAAGGAT TTCCTGCTCA CCTAGTGAAT  
 nArgIleTrp LeuGluGlyPhe AlaAlaAsp LeuValAsn  
 841 ATCATCCCTT CTCGCGCTT TCCCTGGAC AGTGATTTCG  
 IleIleProSer LeuIhrPhe LeuLeuAsp SerAspLeuG  
 881 AGCTCTCTCA GAAAGCATG AATTCCTAC GCATGTGTT  
 LuIhrLeuLys LysSerMET LysPheTyrArg ThrValPh  
 921 TCGAGTCCAT CAAACTCTT TCGGAGATT AGCTAGGAC  
 eGlyValAsp GluIhrSerLeu GlnArgLeu AlaArgAsp  
 961 TCGGAATAG AGGTGGTCA CGTGGAGCC ATGATAAAAT  
 TrpGluIleGlu ValAspGln ValGluAla METIleLysS  
 1001 CTCCTCCCTT GTTCAAACT ACAGATGAG AAACAATACA  
 erProAlaVal PheLysPro ThrAspGluGlu ThrIleGI  
 1041 AGAAGGCTT TCAAGATATA TTCAGGATT CTGTTCGCT  
 nGluArgLeu SerArgTyrIle GlnGluPhe CysLeuAla  
 1081 AATGGTACT TACTTCTTA AATAGTTTT CTAAAGAAA  
 AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI  
 1121 TATTTTACT GAAATATAT TTCCTGACA TGGTGACTCA  
 lePheTyrLeu LysTyrTyr PheLeuAspMET ValThrGI  
 1161 CGATGCTAAA ACTCTCTTA AAGAGATAG TTAAAGAAC  
 uAspAlaLys ThrLeuLeuLys GluIleCys LeuArgAsn  
 1201 PG

FIG. 4 (sheet 2 of 2)

FIG. 5



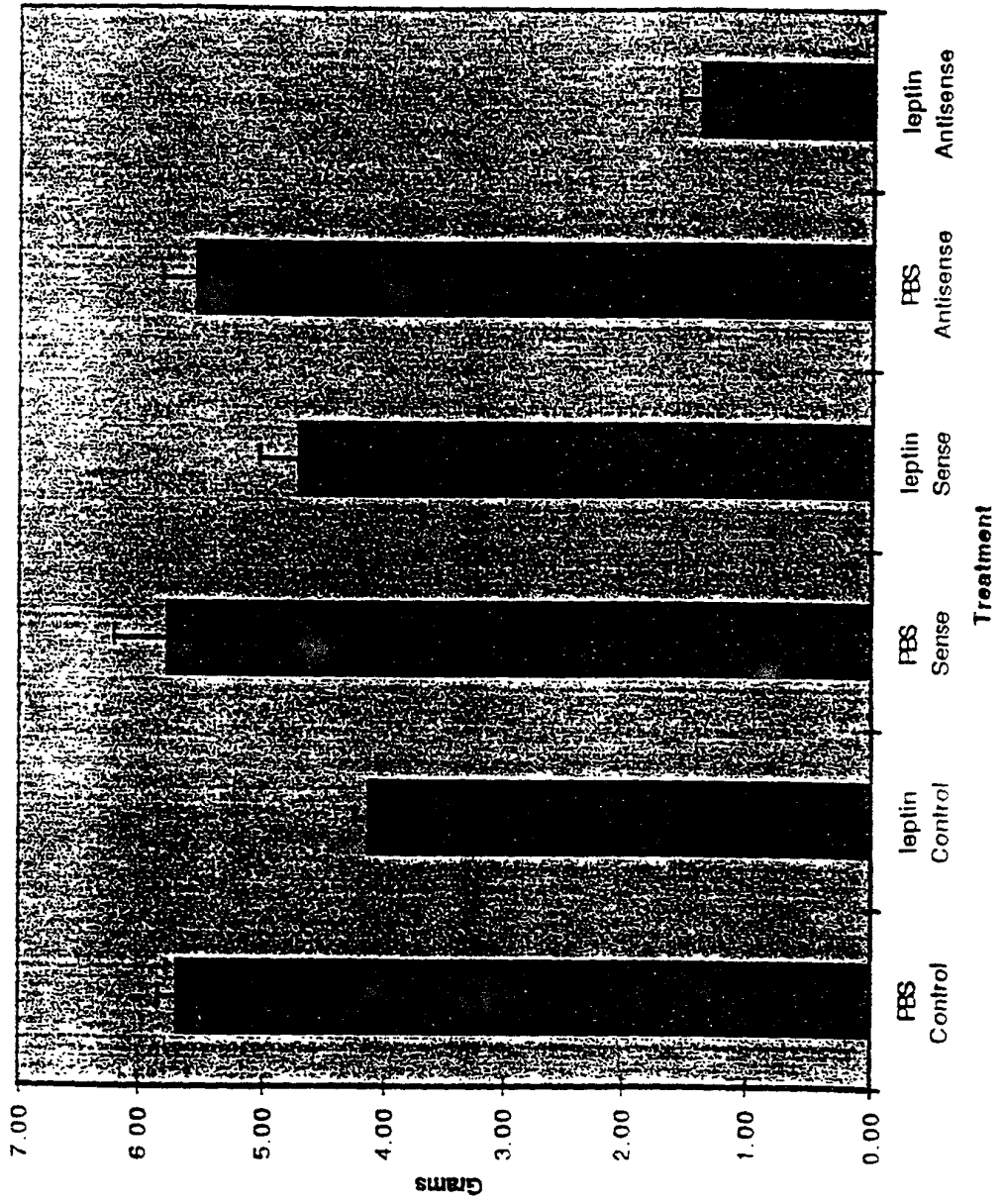


FIG. 6

5'

ACGCGTCCGCGCAGCGGCAGCGGCAGCAGCGGCAACAAGTGCCGGAGGCTA  
GCAGAGCCAAGCCGGAGCAGTCCCTGCCGCCGACACCGCCGGGGCCCGCCGTC  
CGGGGCGCCGCGCATGGAGCGTGAGCTGCCGCCGGTCGCCGGGCTGAGCCGC  
GCGGAGCGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC  
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAAT**T**GAGTGTTGGA  
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA  
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG  
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG  
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT  
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG  
CCATCTGAACTACTGCGAACCTGACCTGAGGGTCACGTCGGTGGTTACGGGT  
TTTAACAACCTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG  
CAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT  
TGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAATC  
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGA  
GTCTTCCTGCTGGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAG  
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA  
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG  
TAAGTACTTCCTGCCCAGACACTGAGTTTGTGTTTCAAGGGCGATGACGATGTT  
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA  
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG  
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC  
ACCCTATGCAGGGGGGAGGGGGGTTTCTCTACTCCGGCCACCTGGCCCTGAGG  
CTGTACCATATCACTGACCAGGTCCATCTCTACCCCATGATGACGTTTATAC  
TGGAATGTGCCTTCAGAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTC

AGGACATTTGATATCGAGGAGAAAAACAAAAATAACATCTGCTCCTATGTAG  
ATCTGATGTTAGTACATAGTAGAAAACCTCAAGAGATGATTGATATTTGGTCT  
CAGTTGCAGAGTGCTCATTTAAAATGCT**T**AAAATAGATACAAACTCAATTTKG  
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT  
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATACCCATTTANGGCC  
TCTAANCCTTCATTTGNACTCACGTGAAGAAGGGAAAGCGGGAGAAGGTAAT  
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA  
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE  
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN  
NLPDRFKDFLLYLRCRNYSLIDQPDKCAKKPFLLAIAKSLTPHFARRQAIRESWG  
QESNAGNQTVVRVFLLGQTPPEDNHPDLSDMLKFESEKHQDILMWNRYRDTFFNL  
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDV  
IHNAGPHRDKKLKYYIPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY  
PIDDVYTGMCCLQKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM  
IDIWSQLQSAHLKC

START

201 CCCCCCCCCCGGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGTGGGACGT 260  
 5 CCCCCCCCCCGGAGCTGGAGGTGTCCCTAGACAAGGTATGAGAGATGAGTGTGGGGCGT 64

351 CGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTATTTTATTATG 320  
 65 CGAAGAGTCAAGTTGCTGGGCATCCTGATGATGGCAAATGTCTTCATTATTTGATTGTG 124

321 GAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGGGAAGTAATAATACCCAAA 380  
 125 GAAGTCTCCAAAACAGTAGCCAAGACAAAAATGGAAAAGGGAGGAGTAATAATCCCGAAA 184

381 GAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGGAACCGAGAGCAAGAGAAG 440  
 185 GAGAAGTTCTGGAAGCCACCCAGCACTCCCGGGCATACTGGAACAGGGAACAGGAGAAG 244

441 CTGAACCGGGCAGTACAACCCCATCCTGAGCATGCTGACCAACCAGACGGGGGAGGGGGC 500  
 245 CTGAACAGGTGGTACAATCCCATCTTGAACAGGGTGGCCAATCAGACAGGGGAGCTAGCC 304

501 AGGCTCTCCAATATAAGCCATCTGAACCTGCGAACCTGACCTGAGGGTCACGTGGGTG 560  
 305 ACATCTCCAAACACAAGTCACCTGAGCTATTGTGAACAGACTCGACGGTCATGACAGCT 364

561 GTTACGGGTTTTTAACAACCTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGC 620  
 365 GTGACAGATTTTAATAATCTGCCGGACAGATTTAAAGACTTTCTCTGTATTTGAGATGC 424

621 CGCAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCTTGTG 680  
 425 CGGAATTACTCGCTGCTTATAGATCAACCGAAGAAATGTGCAAAGAAGCCCTTCTTACTA 484

681 CTGGCGATTAAAGTCCCTCACTCCACATTTTCCAGAAGGCAAGCAATCCGGGAATCCTGG 740  
 485 TTGGCGATAAAGTCCCTCATTCACATTTTCCAGAAGGCAAGCAATCCGGGAGTCTTGG 544

741 GGCCAAGAAAGCAACGCAGGGAACCAACCGGTGGTGGAGTCTTCCTGCTGGGCCAGACA 800  
 545 GGCCGAGAAACCAACGTAGGGAACCAGACAGTAGTGAGGGTCTTCCTGTTGGGCAAGACA 604

801 CCCCCAGAGGACAACCACCCGACCTTTTCTAGATATGCTGAAATTTGAGAGTGAGAAGCAC 860  
 605 CCCCCAGAGGACAACCACCTGACCTTTTCCGACATGCTTAAGTTTGAGAGTGACAAGCAC 664

861 CAAGACATTCTTATGTGGAACCTACAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTG 920  
 665 CAGGACATCCTCATGTGGAACCTATAGAGACACATTCTTCAACCTGTCCCTGAAGGAAGTG 724

921 CTGTTTCTCAGGTGGGTAAAGTACTTCCTGCCCAGACACTGAGTTTGTGTTTCAAGGGCGAT 980  
 725 CTGTTTCTTAGGTGGGTGAGCACTTCCTGTCCAGACGAGAGTTTGTCTTCAAGGGCGAT 784

981 GACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACC 1040  
 785 GATGACGTGTTTGTGAACACCCATCACATCCTTAATTACTTGAATAGCTTATCCAAGAGC 844

1041 AAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGGGATAAG 1100  
 845 AAAGCCAAAGACTTGTTCATAGGTGACGTGATCCACAATGCTGGGCCTCACCGGGATAAG 904

FIG. 9 (10F2)



	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVRVF  
LYLRCRNYSLIDQPKKCAKKPFLLLAIKSLIPHFARRQAIRESWGRETNVGNQTVVRVF  
\*\*\*\*\* \*:.\*\*\*\*\*\*

VFKGDDDDVFVNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLKYYIPEVVYSGLY  
VFKGDDDDVFVNTHHILNYLNSLSKSKAKDLFIGDVIHNAGPHRDKKLKYYIPEVFYTG  
\*\*\*\*\* : : :

PPYAGGGGFLYSGHLALRLYHITDOVHLYPIDDVYTGMC LQKLGLVPEKHKGFRTFDIEE  
PPYAGGGGFLYSGPLALRLYSATSRVHLYPIDDVYTGMC LQKLGLVPEKHKGFRTFDIEE  
\*\*\*\*\* ~\*\*\*\*\*

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC  
KNKKNICSYIDLMLVHSRKPQEMIDIWSQLQSPNLKC  
\*\*\*\*\*.\*\*\*\*\*.\*\*\*\*\* \*\*\*\*\*.\*\*\*

FIG 10

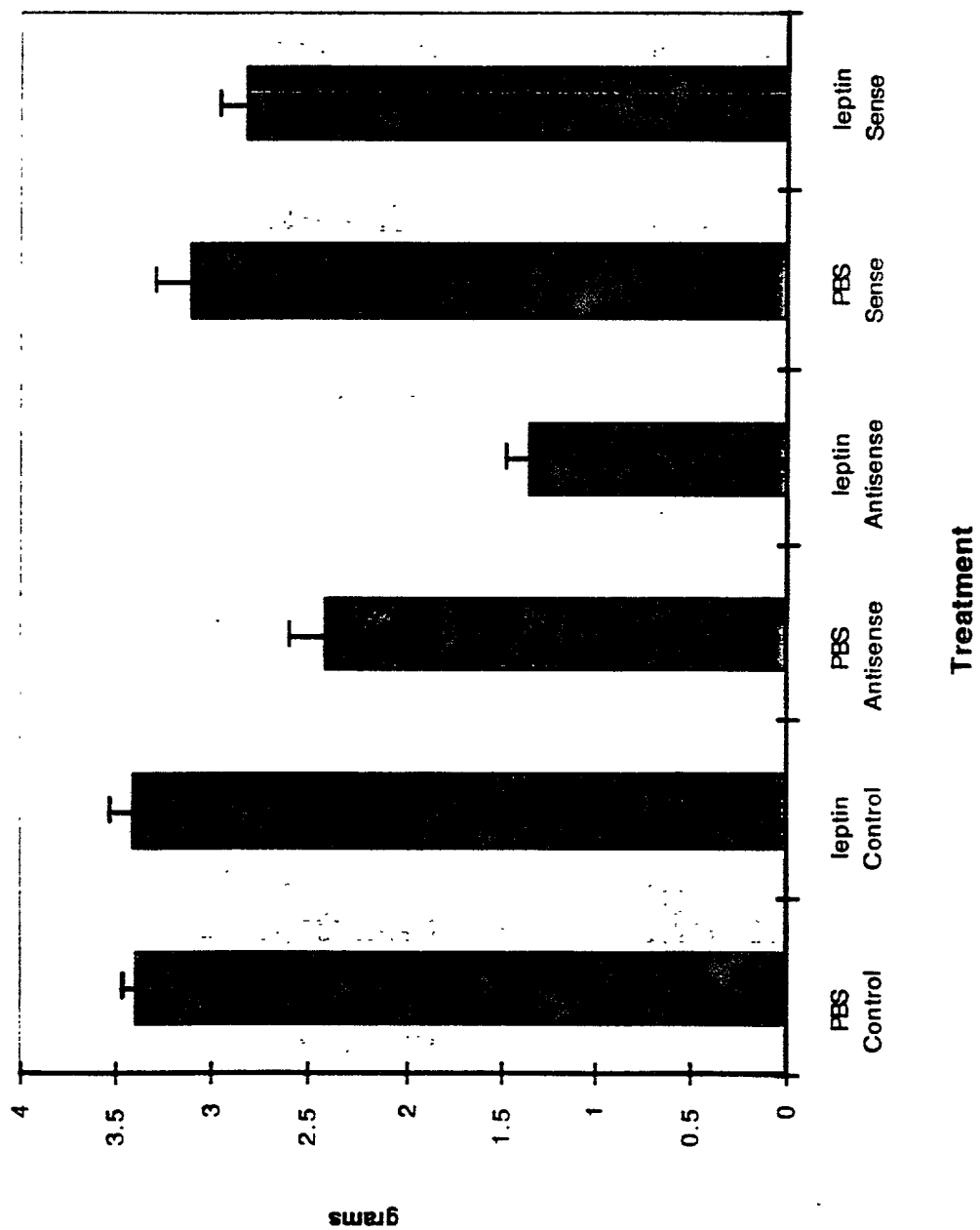


Fig. 11